RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/600,070 A

Source: IFW/16

Date Processed by STIC: 5-26-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
            http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 10/600,070A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .); this will prevent "wrapping."

2 ___ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers: use space characters, instead.

4 ___ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length — Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<22> section that some may be missing

6 ___ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<22> section to be missing from amino acid sequence(s) ___. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<22> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<22> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences (OLD RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences

8 ___ Skipped Sequences (NEW RULES) — Sequence(s) **8** missing. If intentional please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.821 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <22> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ___ Invalid <213> Response — Per 1.821 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence or scientific name (Genus/species). <220>-<22> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220> — Sequence(s) ___ missing the <220> feature and associated numeric identifiers and responses. Use of <220> to <22> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <22> section (See "Federal Register," 06/01/1998, Vol 63, No 104, pp. 29631-32) (See 1.821 of Sequence Rules)

12 ___ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFW16

RAW SEQUENCE LISTING   DATE: 05/26/2005
PATENT APPLICATION: US/10/600,070A   TIME: 12:34:01

        Input Set : A:\08153.ST25.txt
        Output Set: N:\CRF4\05262005\J600070A.raw

  3 <110> APPLICANT: Osteryoung, Katherine W.
  4   Vitha, Stanislav
  5   Koksharova, Olga A.
  6   Gao, Hongo
  8 <120> TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods
of
  9   Use
 11 <130> FILE REFERENCE: MSU-08153
 13 <140> CURRENT APPLICATION NUMBER: 10/600,070A
 14 <141> CURRENT FILING DATE: 2003-06-20
 16 <160> NUMBER OF SEQ ID NOS: 208
 18 <170> SOFTWARE: PatentIn version 3.3

Does Not Comply
Corrected Diskette Needed
(Pg 1-2)

ERRORED SEQUENCES

    811 <210> SEQ ID NO: 8   ?
    812 <211> LENGTH: 0   ?
    813 <212> TYPE: DNA
    814 <213> ORGANISM: Artificial Sequence
    816 <220> FEATURE:
    817 <223> OTHER INFORMATION: Synthetic
    820 <220> FEATURE:
    821 <221> NAME/KEY: misc_feature
    822 <223> OTHER INFORMATION: Intentionally omitted.
    824 <400> SEQUENCE: 8
E--> 824 8   *See error explanation on page 2.*

<210>   8   ⟵ ? pls see item # 8 on error summary sheet,
<211>   0
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Synthetic

<220>
<221>   misc feature   ⟵ whenever <221> is shown, <222> must be inserted.
<223>   Intentionally omitted.   ⟵ delete

<400>   8
<210>   9
<211>   2406
<212>   DNA
<213>   Arabidopsis thaliana

<400>   9

insert space

IF this sequence WAS intentionally skipped, pls see item # 8 on error summary sheet for skipped sequence format.

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY   DATE: 05/26/2005
PATENT APPLICATION: **US/10/600,070A**   TIME: 12:34:03

Input Set : **A:\08153.ST25.txt**
Output Set: **N:\CRF4\05262005\J600070A.raw**

L:824 M:301 E: (44) No Sequence Data was Shown, SEQ ID:8
L:7849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:132 after pos.:120
M:341 Repeated in SeqNo=132
L:8035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:60
L:8134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:144 after pos.:120
M:341 Repeated in SeqNo=144
L:8195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:146 after pos.:0
M:341 Repeated in SeqNo=146
L:8235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:147 after pos.:0
M:341 Repeated in SeqNo=147
L:11295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174 after pos.:0
M:341 Repeated in SeqNo=174
L:11352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:175 after pos.:480
L:11514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:182 after pos.:0
L:11568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:184 after pos.:0
L:13263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:198 after pos.:600
L:13300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:199 after pos.:600
L:13368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:201 after pos.:600
L:13594 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:207 after pos.:0